Amendments to the Claims:

1-30 (canceled).

31. (currently amended) A method for predicting the likelihood that a colon cancer patient ~~diagnosed with an EGFR-expressing colon cancer~~ will respond to treatment with an EGFR inhibitor, comprising determining the normalized level of ~~prognostic~~ predictive RNA transcripts or their products in a sample comprising EGFR-expressing cancer cells obtained from said patient, wherein the ~~prognostic~~ predictive transcripts are the transcript of ~~HER2; STK15; SURV; and TFRC~~ LAMC2 or GPC3 wherein ~~the~~ a higher normalized level of ~~TFRC~~ LAMC2 or the corresponding gene product, ~~when above a defined expression threshold value,~~ indicates that the patient will ~~is likely to~~ show ~~resistance~~ a decreased likelihood of response to treatment with an EGFR inhibitor, and ~~the~~ a higher normalized level of GPC3 ~~HER2; STK15; SURV~~; or the corresponding gene product, ~~when above a defined expression threshold value~~, indicates that the patient will ~~is likely to~~ show an increased likelihood of response ~~respond well~~ to treatment with an EGFR inhibitor.

32-34 (canceled)

35. (previously presented) The method of claim 31 wherein said sample is a tissue sample.

36. (currently amended) The method of claim 35 wherein the tissue sample is fixed, paraffin-embedded, or fresh, or frozen.

37. (currently amended) The method of claim 35 wherein the tissue sample is derived from fine needle, core, or other types of biopsy.

38. (currently amended) The method of claim 31 further comprising the step of preparing a report comprising a statement whether the patient is likely to respond ~~well~~ to treatment with an EGFR inhibitor.

39. (canceled)

40. (currently amended) A method comprising treating a patient diagnosed with an EGFR-expressing colon cancer and determined to have elevated normalized expression of the RNA transcripts of GPC3 gene ~~HER2; STK15; and SURV; genes~~, or the corresponding gene products in said cancer, or decreased normalized expression of the RNA transcripts of ~~TFRC~~ LAMC2 gene, or the corresponding gene products, with an effective amount of an EGFR-inhibitor~~, wherein for each gene elevated or decreased normalized expression is determined relative to a defined expression threshold~~.

41. (currently amended) The method of claim 31 wherein the level of predictive RNA transcript or expression product thereof is determined using an ~~An~~ array comprising polynucleotides hybridizing to the following genes: LAMC2 and GPC3 ~~HER2; STK15; SURV; and TFRC~~; immobilized on a solid surface.

42. (currently amended) The method of ~~array of~~ claim 41 wherein said polynucleotides are cDNAs.

43. (currently amended) The method ~~array~~ of claim 42 wherein said cDNAs are about 500 to about 5000 bases.

44. (currently amended) The method ~~array~~ of claim 41 wherein said polynucleotides are oligonucleotides.

45. (currently amended) The method ~~array~~ of claim 44 wherein said oligonucleotides are about 20 to 80 bases long.

46. (currently amended) The method ~~array~~ of claim 45 wherein the array ~~which~~ comprises about 330,000 oligonucleotides.

47. (currently amended) The method ~~array~~ of claim 41 wherein said solid surface is glass.

48-50. (canceled)

51. (currently amended) The method of claim 35 ~~31~~, wherein RNA is isolated from said fixed, paraffin-embedded tissue by a procedure comprising:

(a) incubating one or more sections ~~a section~~ of said fixed, paraffin-embedded tissue specimen at a temperature of about 56 °C to 70 °C in a lysis buffer, in the presence of a protease, without prior dewaxing, to form a lysis solution;

(b) cooling the lysis solution to a temperature where the wax solidifies; and

(c) isolating the nucleic acid from said cooled lysis solution.

52. (currently amended) The method of claim 31 comprising the use of a [[A]] kit comprising one or more of (1) extraction buffer/reagents for extracting mRNA from a sample and protocol; (2) reverse transcription buffer/reagents and protocol; and (3) qPCR buffer/reagents and protocol suitable for performing the method of claim 31.

53-55 (canceled)

56. (currently amended) A method of using ~~HER2, STK15, SURV and TFRC~~ LAMC2 or GPC3 genes or gene products to predict the likelihood that a patient diagnosed with an EGFR -expressing colon cancer will respond to treatment with an EGFR inhibitor, comprising:

(a) predicting a decreased likelihood of response if the expression level of ~~TFRC~~ LAMC2 gene or the ~~corresponding expression~~ gene product is elevated in said subject, and

(b) predicting an increased likelihood of response if the expression level of GPC3 gene ~~HER2, URV and STK15~~, or the ~~corresponding expression~~ gene product is ~~products are~~ elevated in said subject.

57. (currently amended) A method for predicting the likelihood that a patient diagnosed with an EGFR -expressing colon cancer will respond to treatment with an EGFR inhibitor, comprising:

identifying evidence of differential expression ~~HER2, STK15, SURV and TFRC~~ of LAMC2 or GPC3 genes or gene products, wherein

(a) evidence of increased expression of ~~TFRC~~ LAMC2 indicates that said subject will ~~is expected to~~ show a decreased likelihood of response ~~resistance~~ to treatment with an EGFR inhibitor, and

(b) evidence of increased expression of GPC3 ~~HER2, SURV and STK15~~ indicates that said subject will ~~is expected to~~ show an increased likelihood of response ~~respond well~~ to treatment with an EGFR inhibitor.

58. (canceled)

59. (currently amended) The method ~~array~~ of claim 31 ~~58~~, wherein said polynucleotides from said genes comprise modified and unmodified polynucleotides.

60. (currently amended) The method of claim 31 ~~1~~, further comprising determining the normalized level of one or more prognostic RNA transcripts or their products in said sample, wherein the prognostic transcript is the transcript of one or more genes selected from the group consisting of: Bak; Bclx; BRAF; BRK; Cad17; CCND3; CCNE1; CCNE2; CD105; CD9; COX2; DIABLO; ErbB3; EREG; FRP1; ~~GPC3;~~ GUS; HER2; HGF; ID1; ITGB3; PTPD1; RPLPO; STK15; SURV; TERC; TGFBR2; TITF1; XIAP; CA9; CD134; CD44E; CD44v3; CD44v6; CDC25B; CGA; DR5; GRO1; KRT17; ~~LAMC2;~~ P14ARF; PDGFB; PLAUR; PPARG; RASSF1; RIZ1; Src; TFRC and UPA, wherein the increased normalized level of one or more of CA9; CD134; CD44E; CD44v3; CD44v6; CDC25B; CGA; DR5; GRO1; KRT17; ~~LAMC2;~~ P14ARF; PDGFB; PLAUR; PPARG; RASSF1; RIZ1; Src; TFRC and UPA, or the corresponding gene product, ~~when above a defined expression threshold value,~~ indicates that the patient will ~~is likely to~~ show a decreased likelihood of response ~~resistance~~ to treatment with an EGFR inhibitor, and the increased normalized level of one or more of Bak; Bclx; BRAF; BRK; Cad17; CCND3; CCNE1; CCNE2; CD105; CD9; COX2; DIABLO; ErbB3; EREG; FRP1; ~~GPC3;~~ GUS; HER2; HGF; ID1; ITGB3; PTPD1; RPLPO; STK15; SURV; TERC; TGFBR2; TITF1; and XIAP, or the corresponding gene product~~, when above a defined expression threshold value,~~ indicates that the patient will ~~is likely to respond well~~ show an increased likelihood of response to treatment with an EGFR inhibitor.

61. (new) The method of claim 31, further comprising determining the normalized level of prognostic RNA transcripts LAMC2 and GPC3 or their products in said sample.